

DE #10



PCT

RAW SEQUENCE LISTING

DATE: 10/16/2003

PATENT APPLICATION: US/10/009,571

TIME: 11:20:06

Input Set : A:\PA90631US.ST25.txt

Output Set: N:\CRF4\10162003\J009571.raw

ENTERED

3 <110> APPLICANT: Dear, Neil T.
 5 <120> TITLE OF INVENTION: NOVEL CALPAINS AND THE USE THEREOF
 7 <130> FILE REFERENCE: PA90631US-01938/GRI
 9 <140> CURRENT APPLICATION NUMBER: US 10/009,571
 C--> 10 <141> CURRENT FILING DATE: 2003-03-17
 12 <150> PRIOR APPLICATION NUMBER: DE 19928021.5
 13 <151> PRIOR FILING DATE: 1999-06-18
 15 <160> NUMBER OF SEQ ID NOS: 2
 17 <170> SOFTWARE: Patentln Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2338
 21 <212> TYPE: DNA
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 40 Met Val Ala His
 41 1
 43 ata aac aac agc cgg ctc aag gcc aag ggc gtg ggc cag cac gac aac 163
 44 Ile Asn Asn Ser Arg Leu Lys Ala Lys Gly Val Gly Gln His Asp Asn
 45 5 10 15 20
 47 gcc cag aac ttt ggt aac cag agc ttt gag gag ctg cga gca gcc tgt 211
 48 Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu Arg Ala Ala Cys
 49 25 30 35
 51 cta aga aag ggg gag ctc ttc gag gac ccc tta ttc cct gct gaa ccc 259
 52 Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe Pro Ala Glu Pro
 53 40 45 50
 55 agc tca ctg ggc ttc aag gac ctg ggc ccc aac tcc aaa aat gtg cag 307
 56 Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser Lys Asn Val Gln
 57 55 60 65
 59 aac atc tcc tgg cag cgg ccc aag gat atc ata aac aac cct cta ttc 355
 60 Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn Asn Pro Leu Phe
 61 70 75 80
 63 atc atg gat ggg att tct cca aca gac atc tgc cag ggg atc ctc ggg 403

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64 Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln Gly Ile Leu Gly
65 85 90 95 100
67 gac tgc tgg ctg ctg gct gcc atc ggc tcc ctt acc acc tgc ccc aaa 451
68 Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr Thr Cys Pro Lys
69 105 110 115
71 ctg cta tac cgc gtg gtg ccc aga gga cag agc ttc aag aaa aac tat 499
72 Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe Lys Lys Asn Tyr
73 120 125 130
75 gct ggc atc ttc cat ttt cag att tgg cag ttt gga cag tgg gtg aac 547
76 Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly Gln Trp Val Asn
77 135 140 145
79 gtg gtg gta gat gac cgg ctg ccc aca aag aat gac aag ctg gtg ttt 595
80 Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp Lys Leu Val Phe
81 150 155 160
83 gtg cac tca acc gaa cgc agt gag ttc tgg agt gcc ctg ctg gag aag 643
84 Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala Leu Leu Glu Lys
85 165 170 175 180
87 gcg tat gcc aag ctg agt ggg tcc tat gaa gca ttg tca ggg ggc agt 691
88 Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu Ser Gly Gly Ser
89 185 190 195
91 acc atg gag ggc ctt gag gac ttc aca gga ggc gtg gcc cag agc ttc 739
92 Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val Ala Gln Ser Phe
93 200 205 210
95 caa ctc cag agg ccc cct cag aac ctg ctc agg ctc ctt agg aag gcc 787
96 Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu Leu Arg Lys Ala
97 215 220 225
99 gtg gag cga tcc tcc ctc atg ggt tgc tcc att gaa gtc acc agt gat 835
100 Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu Val Thr Ser Asp
101 230 235 240
103 agt gaa ctg gaa tcc atg act gac aag atg ctg gtg aga ggg cac gct 883
104 Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val Arg Gly His Ala
105 245 250 255 260
107 tac tct gtg act ggc ctt cag gat gtc cac tac aga ggc aaa atg gaa 931
108 Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg Gly Lys Met Glu
109 265 270 275
111 aca ctg att cgg gtc cgg aat ccc tgg ggc cgg att gag tgg aat gga 979
112 Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile Glu Trp Asn Gly
113 280 285 290
115 gct tgg agt gac agt gcc agg gag tgg gaa gag gtg gcc tca gac atc 1027
116 Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val Ala Ser Asp Ile
117 295 300 305
119 cag atg cag ctg ctg cac aag acg gag gac ggg gag ttc tgg atg tcc 1075
120 Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu Phe Trp Met Ser
121 310 315 320
123 tac caa gat ttc ctg aac aac ttc acg ctc ctg gag atc tgc aac ctc 1123
124 Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu Ile Cys Asn Leu
125 325 330 335 340
127 acg cct gat aca ctc tct ggg gac tac aag agc tac tgg cac acc acc 1171
128 Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr Trp His Thr Thr

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131	ttc tac gag ggc agc tgg cgc aga ggc agc tcc gca ggg ggc tgc agg						1219
132	Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala Gly Gly Cys Arg						
133		360		365		370	
135	aac cac cct ggc acg ttc tgg acc aac ccc cag ttt aag atc tct ctt						1267
136	Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe Lys Ile Ser Leu						
137		375		380		385	
139	cct gag ggg gat gac cca gag gat gac gca gag ggc aat gtt gtg gtc						1315
140	Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly Asn Val Val Val						
141		390		395		400	
143	tgc acc tgc ctg gtg gcc cta atg cag aag aac tgg cgg cat gca cgg						1363
144	Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp Arg His Ala Arg						
145	405		410		415		420
147	cag cag gga gcc cag ctg cag acc att ggc ttt gtc ctc tac gcg gtc						1411
148	Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val Leu Tyr Ala Val						
149		425		430		435	
151	cca aaa gag ttt cag aac att cag gat gtc cac ttg aag aag gaa ttc						1459
152	Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu Lys Lys Glu Phe						
153		440		445		450	
155	ttc acg aag tat cag gac cac ggc ttc tca gag atc ttc acc aac tca						1507
156	Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile Phe Thr Asn Ser						
157		455		460		465	
159	cgg gag gtg agc agc caa ctc cgg ctg cct ccg ggg gaa tat atc att						1555
160	Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly Glu Tyr Ile Ile						
161		470		475		480	
163	att ccc tcc acc ttt gag cca cac aga gat gct gac ttc ctg ctt cgg						1603
164	Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp Phe Leu Leu Arg						
165	485		490		495		500
167	gtc ttc acc gag aag cac agc gag tca tgg gaa ttg gat gaa gtc aac						1651
168	Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu Asp Glu Val Asn						
169		505		510		515	
171	tat gct gag caa ctc caa gag gaa aag gtc tct gag gat gac atg gac						1699
172	Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu Asp Asp Met Asp						
173		520		525		530	
175	cag gac ttc cta cat ttg ttt aag ata gtg gca gga gag ggc aag gag						1747
176	Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly Glu Gly Lys Glu						
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179	ata ggg gtg tat gag ctc cag agg ctg ctc aac agg atg gcc atc aaa						1795
180	Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg Met Ala Ile Lys						
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183	ttc aaa agc ttc aag acc aag ggc ttt ggc ctg gat gct tgc cgc tgc						1843
184	Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp Ala Cys Arg Cys						
185	565		570		575		580
187	atg atc aac ctc atg gat aaa gat ggc tct ggc aag ctg ggg ctt cta						1891
188	Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys Leu Gly Leu Leu						
189		585		590		595	
191	gag ttc aag atc ctg tgg aaa aaa ctc aag aaa tgg atg gac atc ttc						1939
192	Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp Met Asp Ile Phe						
193		600		605		610	

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196 Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn Ser Tyr Glu Met
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199 cgc ctg gtt att gag aaa gca ggc atc aag ctg aac aac aag gta atg 2035
200 Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn Asn Lys Val Met
201      630      635      640
203 cag gtc ctg gtg gcc agg tat gca gat gat gac ctg atc ata gac ttt 2083
204 Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Asp Leu Ile Ile Asp Phe
205 645      650      655      660
207 gac agc ttc atc agc tgt ttc ctg agg cta aag acc atg ttc aca ttc 2131
208 Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr Met Phe Thr Phe
209      665      670      675
211 ttt cta acc atg gac ccc aag aat act ggc cat att tgc ttg agc ctg 2179
212 Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile Cys Leu Ser Leu
213      680      685      690
215 gaa cag tgg ctg cag atg acc atg tgg gga tag aggcgctgta ggagcctggt 2232
216 Glu Gln Trp Leu Gln Met Thr Met Trp Gly
217      695      700
219 catctctacc agcagcagca gcagcgaggt tctagcccag gaggggtgggg tgcttcttgt 2292
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237      35      40      45
239 Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser
240      50      55      60
242 Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn
243 65      70      75      80
245 Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln
246      85      90      95
248 Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr
249      100      105      110
251 Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe
252      115      120      125
254 Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly
255      130      135      140
257 Gln Trp Val Asn Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp
258 145      150      155      160
260 Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala
261      165      170      175
263 Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu
264      180      185      190

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272 Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu
273 225      230      235      240
275 Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val
276      245      250      255
278 Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg
279      260      265      270
281 Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile
282      275      280      285
284 Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val
285      290      295      300
287 Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu
288 305      310      315      320
290 Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu
291      325      330      335
293 Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr
294      340      345      350
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297      355      360      365
299 Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe
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302 Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly
303 385      390      395      400
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306      405      410      415
308 Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val
309      420      425      430
311 Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu
312      435      440      445
314 Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile
315      450      455      460
317 Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly
318 465      470      475      480
320 Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
321      485      490      495
323 Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
324      500      505      510
326 Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
327      515      520      525
329 Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
330      530      535      540
332 Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
333 545      550      555      560
335 Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
336      565      570      575
338 Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys

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VERIFICATION SUMMARY

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DATE: 10/16/2003

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